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# **Genome Wide Association Study on beef production Traits in Marchigiana**

## **Cattle breed**

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24 **Summary**

25 A genome-wide association study was carried out on a sample of Marchigiana breed cattle to detect  
26 markers significantly associated with carcass and meat traits. Four hundred and nine young bulls  
27 from 117 commercial herds were genotyped by Illumina 50K BeadChip assay. Eight growth and  
28 carcass traits (average daily gain, carcass weight, dressing percentage, body weight, skin weight,  
29 shank circumference, head weight, carcass conformation) and two meat quality traits (pH at  
30 slaughter and pH 24 hours after slaughter) were measured. Data were analyzed with a linear mixed  
31 model that included fixed effects of herd, slaughter date, fixed covariables of age at slaughter and  
32 SNP genotype, and random effects of herd and of animal. A permutation test was performed to  
33 correct SNP genotype significance level for multiple testing. A total of 96 SNPs were  
34 significantly associated at genome-wide level with one or more of the considered traits. Gene search  
35 was performed on genomic regions identified on the basis of significant SNP position and level of  
36 linkage disequilibrium. Interesting loci affecting lipid metabolism (*SOAT1*), bone (*BMP4*) and  
37 muscle (*MYOF*) biology were highlighted. These results may be useful to better understand the  
38 genetic architecture of growth and body composition in cattle.

39  
40 **Keywords:** SNP chip, GWAS, bovine, productive traits

41  
42 **Introduction**

43 The recent availability of high throughput SNP platforms for several livestock species has  
44 revitalized the search for DNA markers associated to phenotypic variation in complex traits of  
45 economic importance (Bush and Moore 2012). Genome-wide association studies (GWAS)  
46 represent a first step toward the understanding of molecular and cellular mechanisms underlying  
47 phenotypic expression of complex traits (Jiang *et al.* 2010; Korte and Farlow 2013).

48 Genomic approaches are expected to have a great impact on traits that are difficult and expensive to  
49 measure. An example are *post-mortem* traits in beef cattle. Dressing percentage, carcass  
50 composition, and meat quality are difficult to obtain and relate to animals retained for selection.  
51 Recent GWAS studies have detected associations between SNPs and beef traits, suggesting  
52 *myostatin*, *DGAT1* and *leptin receptor* as candidate genes (Jiang *et al.* 2010).

53 Local beef breeds are important for typical production systems and for crossbreeding with  
54 specialized breeds. GWAS carried out on local breeds may provide useful insights in the genetic  
55 determinism of meat traits by picking up genetic variation no longer detectable in cosmopolitan  
56 breeds. In Italy there are several local beef cattle breeds. They differ in selection history, trait  
57 phenotypic expression, and genetic background (Sorbolini *et al.*, 2015). The Marchigiana breed is a  
58 typical example. It originated from the Asiatic long-horned (*Bos primigenius*) cattle and moved to  
59 Italy from Central Asian steppes during invasions in the sixth/seventh century C.E. (Trombetta *et*  
60 *al.* 2005). Beef traits were improved by crosses with Chianina and Romagnola cattle in the second  
61 half of the nineteenth century. The current Marchigiana is the result of a breeding program started  
62 after the above mentioned cross-breeding. At present, it is the second beef breed of Italy with about  
63 52,344 hd registered in the Herdbook. It is characterized by a strong adaptability to harsh  
64 environmental conditions, great precocity, fertility and a remarkable aptitude for meat production  
65 (Balasini 1981) due to well-pronounced muscle development and fine bone structure and skin. For  
66 these reasons it has also been exported to countries such as United States, Canada, Brazil,  
67 Argentina and Australia (“<http://www.anabic.it/>”)

68 In the present work, a GWAS was carried out on a sample of 409 Marchigiana young bulls farmed  
69 in commercial herds, genotyped with the Illumina Bovine SNP50 BeadChip. The study was aimed  
70 at identifying chromosome regions harbouring new putative candidate genes affecting meat and  
71 carcass quality traits in beef cattle.

## 73    **Material and Methods**

### 74    Animals and phenotypic data

75    Four hundred and nine Marchigiana young bulls from 117 commercial herds were slaughtered  
76    between 16 and 24 months of age. Phenotypes of ten different growth, carcass and meat quality  
77    traits were recorded at the slaughter house: body weight (BW), average daily gain (ADG), carcass  
78    weight (CW), dressing percentage (DP), skin weight (SW), shank circumference (SC), head weight  
79    (HW), carcass conformation according to the European grid based on muscularity and fat content  
80    (SEUROP) evaluation system (CC), pH at slaughter (pH) and pH 24 hours after slaughter  
81    (pH24h). pH at slaughter and 24h after slaughter were measured on the *longissimus dorsii* muscle  
82    with the HI 99 163 pHmeter (Hanna instruments).

83

### 84    Genotypic data

85    Genomic DNA was extracted from whole blood samples gathered immediately before slaughter  
86    using the NucleoSpin 96 Blood Kit (Macherey-Nagel) according to manufacturer's instructions.  
87    All 409 animals were genotyped using the Illumina 50K BeadChip assay. SNP editing was on call  
88    rate (>99%) and minor allele frequency (>1%). Animals having more than 2,5% of missing  
89    genotypes were discarded. A total of 43,313 markers were retained after edits.

90

### 91    Statistical Analysis

92    Data were analyzed using the following mixed linear model:

$$93 \quad Y = D + bAGE + bSNP + a + h + e \quad [1]$$

94    where:

95    Y = record for the the considered trait;

96    D = fixed effect of slaughter date (46 levels);

97    bAGE = fixed covariable of age at slaughter in months ;

98 bSNP = fixed covariable of SNP genotype (coded as 0, 1, 2 according to the number of second  
99 allele)

100 a = random additive genetic effect of the animal.

101 h = random effect of the herd (114 levels);

102 e = random residual.

103 The animal effect was assumed to be normally distributed  $\sim N(0, G\sigma_a^2)$  where **G** is the genomic  
104 relationship matrix and  $\sigma_a^2$  is the additive genetic variance. **G** was calculated according to  
105 VanRaden (2008) as:

106 
$$G = \frac{ZZ'}{2 \sum p_i(1-p_i)}$$

107 where **Z** is the matrix of individual genotypes scaled by allele frequencies ( $p_i$ ) expressed as  
108 differences from 0.5.

109 A modified version of the experimentwise empirical threshold proposed by Churchill and Doerge  
110 (1994) was used to correct SNP statistical significance for multiple testing. In a first step, single  
111 marker analysis was performed with model [1]. Significant markers ( $P < 0.01$ ) were retained. In the  
112 second step, 10,000 permutations were performed for each significant marker by shuffling SNPs  
113 across animals, while keeping invariant the other factors included in model [1] (Anderson and Ter  
114 Braak 2003). The bottom 5% of  $\alpha$  probabilities of test statistics for each marker (SNP\_ALPHA)  
115 were retained. Then SNP\_ALPHA for all SNPs were put in the same column, and the 5th percentile  
116 was kept as a critical threshold for declaring significant at  $P < 0.05$  tests performed in the first step.  
117 Statistical analyses were performed using SAS 9.2 (SAS/STAT software version 9.2, SAS Institute,  
118 Inc. Cary, NC, USA).

119

120 Putative candidate genes identification

Gene search was performed on chromosome regions defined by positions of significant SNPs according to the sixth draft of bovine genome assembly (UMD3.1/bosTau 6) UCSC Genome Browser Gateway (<http://genome.ucsc.edu/>). Windows of variable amplitude in Mb were defined based on linkage disequilibrium of the specific genomic region (Macciotta *et al.* 2015). For each significant SNP the squared coefficient ( $r^2$ ) statistic with all other SNPs positioned in the same chromosome was calculated (Table S1). Distance between the significant SNP and the furthest SNP having an  $r^2 > 0.10$  was calculated and added upstream and downstream to the position of significant marker. SNP not in LD with other markers were not considered for gene discovery. Finally, specific functional analysis and biological roles of annotated genes were investigated by an accurate literature search and databases consultation such as GeneCards ([www.genecards.org](http://www.genecards.org)), National Centre for Biotechnology Information ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)), Proteinatlas ([www.proteinatlas.org](http://www.proteinatlas.org)). Gene names and symbols were derived from HUGO Gene nomenclature database ([www.genenames.org](http://www.genenames.org)).

134

## 135 **Results**

### 136 Significant SNPs and association analyses

137 A total of 96 SNPs were found to be associated with seven out of ten considered traits (ADG, 138 CW, DP, BW, HW, SC and pH) (Table S1). As an example, figure 1 reports the Manhattan plot for 139 ADG.

140 No significant SNP were found for pH24h, SW and CC. The largest number of significant markers 141 associated with different traits was found on BTA2 (14 SNPs), followed by BTA6 (11 SNPs) and 8 142 (10 SNPs). Chromosomes 9, 11, 12, 18, 19, 23, and 29 showed only one significant marker. BTAs 143 13, and 27 did not show any associated marker.

144 Significant markers of BTA2 were associated with five different traits (ADG, CW, DP, pH, and 145 SC) followed by BTA8 with four (ADG, HW, SC, pH) and 26 with three (HW, SC, pH). Finally, a



total of two SNPs resulted associated with two traits (ADG and BW); rs43272238 on BTA1, and rs41662409 on BTA16.

148

#### Average Daily Gain

Forty-five significant markers were detected for ADG. Chromosome 6 showed the highest number of SNP associated with this trait (10). BTAs 5, 15, 22, 24 and 28 contained only one significant marker associated with ADG. A SNP located on BTA10 between 65,7 and 67,5 Mb (*rs41568676*) flagged a region where the *bone morphogenetic protein 4 (BMP4)* gene maps (Table1). On BTA14 the rs41631408 at 57469150 bp pointed out the *thyrotropin-releasing hormone receptor (THRH)* locus. Other significant markers associated with ADG identified several distinct genes involved primarily in cellular processes such as growth and proliferation (*IFRD1, CGRRF1, TGFB2*), but also genes involved in general metabolic pathways such as (*SPTLC1, UTG1A6* and *UTG1A1*) or specific pathways such as carbohydrate metabolism (*ALDOA*) and lipid metabolism (*SOAT1*) (Table1).

160

#### Shank circumference

Table S1 reports the 13 significant markers found to be associated with SC. After ADG, it was the trait with the highest number of significant associated markers. Three of them were found on BTA14 and two on BTA8. However, no annotated genes were retrieved in the corresponding chromosomal regions.

166

#### Dressing Percentage

Twelve SNPs were found significantly associated with DP. Eight out of 12 were located in a large chromosomal region between 1,0-5,2 Mb on BTA2. These SNPs were in close proximity with a

170 QTL that contains the *myostatin* (*MSTN*) locus and two other genes that have a role in muscle  
171 biology (*SLC40A1* and *COL5A2*.) On BTA9 at 288595 bp from the significant SNP *rs 41662464*  
172 map the *connective tissue growth factor* (*CTGF*), a gene involved in chondrocyte proliferation.

173

#### 174 Carcass Weight

175 In this study, 9 significant markers distributed over seven different autosomes were associated  
176 with CW. Four SNPs were found on BTA5 (Table S1). On BTA2 the SNP *rs109168082* at 129,8  
177 Mb tagged to the *PNRC2*, *GALE* genes (Table 1). On BTA23 the validated mRNA sequence of  
178 *ATP-binding cassette, subfamily F (GCN20), member 1 (ABCF1)* is annotated close to the  
179 *rs110277462* marker.

180

#### 181 Head Weight

182 A total of 7 significant SNPs were associated with HW. BTA7 harbored the largest number of  
183 markers (n = 2) associated with this trait (Table S1) whereas BTAs 5,11,16,20 and 26 showed a  
184 single significant marker.

185

186

#### 187 Body weight

188 A total of 5 significant SNPs were found associated with BW (Table S1). Few annotated genes were  
189 retrieved in the intervals surrounding these SNPs. Three significant markers were shared with other  
190 traits examined in this study. On BTA7, a significant marker (*rs42691441*) associated to the BW  
191 and located at 68,070,311 bp was also associated with HW. The annotated sequence nearest the  
192 marker was the *CCR4-NOT transcription complex, subunit 8 mRNA (CNOT8)*.

193

#### 194 pH at slaughter

195 Five significant markers were found to be associated with pH at slaughter (Table S1). A single  
196 associated SNP was on BTAs 2, 3, 14, 17, and 26. No suggestive genes were found for this trait.

197

## 198 **Discussion**

199 Growth performance and growth-related traits such as body size and weight or average daily gain,  
200 have a crucial role in livestock due to their influence on meat production. Average daily weight gain  
201 is one of the most important traits for assessment of animal growth and it is a component of most  
202 economic indices. In livestock, discovering and understanding genes and molecular mechanisms  
203 underlying differences in ADG could clarify relationships among weight gain and other important  
204 traits such as body composition or feed intake (Santana *et al.* 2014).

205 Marchigiana cattle have been selected for meat production (a trait with a medium to high  
206 heritability) over the last twenty years. Aim of this study was to identify candidate genes associated  
207 with beef production traits in this breed. The total number of significant associations detected in this  
208 GWAS was in general agreement with literature (Snelling *et al.* 2010; Rolf *et al.* 2012).

209 SNPs significantly associated to ADG flagged regions where genes involved in the metabolism of  
210 sugars and lipids are located. This is in general agreement with cattle physiology because these  
211 metabolic pathways may have a significant influence on average daily gain. An interesting  
212 outcome of the present study is represented by the association between ADG and two markers  
213 (*rs41662409* and *rs110397182*) located on BTA 16. These associations underline *Sterol-O-*  
214 *Acyltransferase 1 (SOAT1)* and *transforming growth factor, beta 2 (TGFB2)* genes, respectively. In  
215 particular *SOAT1* was already reported as a candidate gene in beef cattle (Jiang *et al.* 2009). *SOAT1*  
216 encodes for an enzyme that is involved in steroidogenesis and lipogenesis/lipolysis network.

217 Another promising candidate gene for ADG was *TGFB2*. This gene regulates cell proliferation and  
218 differentiation and it was already reported as a locus involved in extracellular matrix organization  
219 of muscle development (Guo *et al.* 2015). Moreover, polymorphisms at *TGFB2* were associated

220 with growth traits in chicken (Mojtaba *et al.* 2013). A significant marker (*rs41631408*) located on  
 221 BTA14 between 57,4-57,5 Mb highlighted the *thyrotropin-releasing hormone receptor (TRHR)*.  
 222 This gene encodes for the receptor responsible of thyrotropin hormone (TRH) release. In mammals  
 223 *THR* is involved in somatotropin (GH) secretion, regulation and activity (Harvey 1990). The  
 224 relationship between blood concentration of GH and growth has long been known and positive  
 225 effects of *THR* on growth and carcass characteristics in beef cattle performances were already  
 226 reported by Enright *et al.* (1993).  
 227 Finally, the marker *rs43395215* found to be associated with ADG tagged a putative  
 228 candidate gene, *interferon-related development regulator (IFRD1)*, involved in adipocyte  
 229 proliferation, growth and differentiation.  
 230 Carcass weight and dressing percentage represent economically important traits for livestock  
 231 production. However, in recent years, meat quality has also received more attention as economically  
 232 important. Phenotypic traits such as tenderness, marbling and unsaturated fat content are  
 233 considered essential in the beef industry. Dressing percentage trait is an estimate of amount of  
 234 saleable product derived from a given carcass (Casas *et al.* 2003). The *MSTN* locus, encoding  
 235 myostatin, is one of the most studied genes in beef cattle (Djari *et al.* 2013). Polymorphism at this  
 236 single autosomal locus causes double muscle phenotype. Several mutations have been previously  
 237 reported in many cattle breeds for *MSTN* (Djari *et al.* 2013). In mammals, polymorphisms in this  
 238 locus result in muscle hyperplasia caused by inactivation of the negative regulator of myogenesis  
 239 (McPherron and Lee 1997). *MSTN* mutations are associated with increased muscle mass, carcass  
 240 yield, meat tenderness and a reduction of collagen content in cattle (Esmailzadeh *et al.* 2008).  
 241 Besides economic benefits, double muscled phenotype implies undesirable consequences such as  
 242 reduced fertility, low calf viability and dystocia (Bellinge *et al.* 2005). A point mutation consisting  
 243 of a G/T transversion in the third exon of *MSTN* has been reported in Marchigiana (Marchitelli *et*  
 244 *al.* 2003). This variant has a rather low frequency in the population, probably due to the careful

245 breeding policy of breeders that want to avoid negative effects on reproduction. However extreme  
246 double-muscling individuals are still observed (Marchitelli *et al.* 2003). Also SNP in the promoter  
247 region of this gene may influence muscularity and therefore DP (Crisà *et al.* 2003). Significant  
248 markers found in this study identify a QTL region where *MSTN* and other neighboring genes such  
249 as *Collagen, type V, alpha 2 (COL5A2)* and *Solute carrier family 40, member A1 (SLC40A1)*  
250 involved in muscle biology and collagen biosynthesis were located. This result is in agreement with  
251 previous reports for beef cattle (Pintus *et al.* 2014, Saatchi *et al.* 2014).

252

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256

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## 258 **References**

259

- 260 1) Anderson M.J., Ter Braak C.J.F. (2003) Permutation tests for multi-factorial analysis of variance.  
261 J. Stat. Comp. Simul., **73**, 85-113.
- 262 2) Balasini D. (1981) Razze bovine da carne. Incroci e loro prospettive. Edagricole.
- 263 3) Bellinge R.H.S., Liberles D.A., Iaschi S.P.A., O'Brian P.A., Tay G.K. (2005) Myostatin and its  
264 implications on animal breeding: a review. Anim. Genet., **36**, 1-6.
- 265 4) Bush W.S., Moore J.H. (2012) Chapter 11: Genome-wide association studies. PLoS Comput.  
266 Biol., **8**, e1002822.

270

271 5) Casas E., Shakelford S.D., Keele J.W., Koohmaraie M., Smith T.P.L., Stone R.T. (2003)  
272 Detection of Quantitative trait loci for growth and carcass composition in cattle. *J Anim. Sci.*, 81,  
273 2976-2983.

274 6) Churchill G.A., Doerge D.R. (1994). Empirical Threshold Values for Quantitative Trait  
275 Mapping. *Genetics.*, **138**, 963-971.

276 7) Crisà A., Marchitelli C., Savarese M.C., Valentini A. (2003) Sequence analysis of myostatin  
277 promoter in cattle. *Cytogenet.Genome Res.*, **102**,. 48-52.

280 8) Djari A., Esquerre D., Weiss B., Martins F., Meersseman C., Boussaha M., Klopp C., Rocha D.  
281 (2013) Gene-based single nucleotide polymorphism discovery in bovine muscle using next-  
282 generation transcriptomic sequencing. *BMC Genomics.*, **14**, 307.

284 9) Enright W.J., Prendiville D.J., Spicer L.J., Striker P.R., Moloney D.P., Mowles T.F., Campbell  
285 R.M. (1993) Effects of growth hormone-releasing factor and (or) thyrotropin-releasing hormone on  
286 growth, feed efficiency, carcass characteristics, and blood hormones and metabolites on beef  
287 heifers. *J. Anim Sci.*, **71**, 2395-2405.

289 10) Esmailizadeh A.K., Bottema C.D., Selick G.S., Verbyla A.P., Morris C.A., Cullen N.G.,  
290 Pitchford W.S. (2008) Effects of the myostatin F94L substitution on beef traits. *J. Anim. Sci.*, **86**,  
291 1038-1046.

292 11) Guo B., Greenwood P.L., Cafe L.M., Zhou G., Zhang W., Dalrymple B.P. (2015)  
293 Transcriptome analysis of cattle muscle identifies potential markers for skeletal muscle growth rate  
294 and major cell types. *BMC Genomics.*, **16**, 177.

296 12) Harvey S. (1990) thyrotropin-releasing hormone: a growth-hormone releasing factor.*J.*  
297 *Endocrinology*, **125**, 345-358.

298  
299 13) Jiang Z., Michal J.J., Chen J., Daniels T.F., Kunej T., Garcia M.D., Gaskin C.T., Busboom J.R.,  
300 Alexander L.J., Wright Jr R.W., MacNeil M.D. (2009) Discovery of novel genetic networks  
301 associated with 19 economically important traits in beef cattle. *Int. J. Biol. Sci.*, **5**, 528-542.

302  
303 13) Macciotta N.P.P., Gaspa G., Bomba L., Vicario D., Dimauro C., Cellesi M., Ajmone- Marsan P.  
304 (2015) Genome-wide association analysis in Italian Simmental cows for lactation curve traits using  
305 a low-density (7K) SNP panel. *J. Dairy Sci.*, **98**, 1-11.

306  
307 14) Marchitelli C., Savarese M.C., Crisà A., Nardone A., Ajmone-Marsan P., Valentini A. (2003)  
308 Double muscling in Marchigiana beef breed is caused by a stop codon in the third exon of *myostatin*  
gene *Mamm Genome.*, **14**, 392-5.

309  
310 15) Mc Pherron A.C., Lee A. C. (1997) Double-muscling in cattle due to mutations in the myostatin  
311 gene. *Proc. Natl. Acad Sci., USA.* 94, 12457-12461.

312  
313 16) Pintus E., Sorbolini S., Albera A., Gaspa G., Dimauro C., Steri R., Macciotta N.P.P. (2014)  
314 Use of locally weighted scatterplot smoothing (LOWESS) regression to study selection signatures  
315 in Piedmontese and Italian Brown cattle breeds. *Anim. Genet.*, **45**, 1-11.

316  
317 17) Rolf M.M, Taylor J.F., Schnabel R.D., McKay S.D., McClure M.C., Nbirthcult S.L., Kerley  
318 M.S.,Weaber R.L. (2012) Genome-wide association analysis for feed efficiency in Angus cattle.  
319 *Anim Genet.*, **43**, 367-374.

320  
321 18) Saatchi M., Schnabel R.D, Taylor J.F., Garrick D. J. (2014) Large-effect pleiotropic or closely  
322 linked QTLsegregate within and across ten US cattle breeds. *BMC Genomics*, **15**, 442-458.

323

324 19) Santana M.H.A., Utsunomya Y.T., Neves H.H.R., Gomes R.C., Gatica J.F., Fukumasu H., Silva  
 325 S.L., Leme P.R., Coutinho L.L., Eler J.P., Ferraz J.B.S. (2014) Genome-wide association study for  
 326 feedlot average daily gain in Nellore cattle (*Bos indicus*), J. Anim. Breed. Genet. **131**, 210-216.  
 327  
 328 20) Snelling W.M., Allan M.F., Keele J.W., Khuen L.A., McDanel T., Smith T.P.L., Sonstegard  
 329 T.S., Thallman R.M., Bennett G.L. (2010) Genome-wide association study of growth in crossbred  
 330 beef cattle. J. Anim. Sci., **88**, 837-848.  
 331  
 332 21) Sorbolini S., Marras G., Gaspa G., Dimauro C., Cellesi M., Valentini A., Macciotta N.P.P  
 333 (2015) Detection of selection signatures in Piemontese and Marchigiana cattle, two breeds with  
 334 similar production aptitudes but different selection histories GSE., **47**, 52-65.  
 335  
 336 22) Trombetta M.F., Mattii S., Sbarra F., Palazzo R., Caimmi D., Falaschini a., Forabosco F.,  
 337 Filippini F. (2005) Observations at slaughtering time: carcass characteristics of Marchigiana beef.  
 338 Preliminary results. Proceedings of the 4<sup>th</sup> World Italian Beef Cattle Congress, Gubbio (Italy) April  
 339 29<sup>th</sup>- May 1<sup>st</sup> 549-554.  
 340  
 341 24) VanRaden P. (2008) Efficient Methods to Compute Genomic Predictions. J. Dairy Sci., **91**,  
 342 4414-4423.  
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 349 Supporting Information



350 Table S1: List of significant markers associated with the traits under study.

351

352 **Tables**

353 **Table 1.**

354

355

356 **Figures**

357 **Figure 1.**

358 **Captions for Tables**

359 **Table 1:** Putative candidate genes associated with *in vivo* and *post mortem* phenotypes under  
360 study.

361

362 **Captions for Figures**

363 **Figure 1.** Genome-wide association study of average daily gain. The dashed line corresponds  
364 to a permutation treshold of 0.05.

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